

SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> *Lawsonia intracellularis* subunit vaccines.

<130> 2004.001

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 2088

<212> DNA

<213> *Lawsonia intracellularis*

<220>

<221> CDS

<222> (16)..(2085)

<400> 1

```

cggaggttga ttact atg agt ctt aca gca gga atg tgg aca ggt gtt tca      51
          Met Ser Leu Thr Ala Gly Met Trp Thr Gly Val Ser
          1             5             10

gga ctt tta agt cat ggc gaa aag atg aat gtt att ggt aat aac ata      99
Gly Leu Leu Ser His Gly Glu Lys Met Asn Val Ile Gly Asn Asn Ile
          15             20             25

gct aac gta aat aca gta ggc ttt aaa ggc caa cgt atg gat ttc gca     147
Ala Asn Val Asn Thr Val Gly Phe Lys Gly Gln Arg Met Asp Phe Ala
          30             35             40

gac ttt att tat caa gat ggc ttt agt act gca ggg att aca caa att     195
Asp Phe Ile Tyr Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile
          45             50             55             60

gga cgt ggt gta ggc att gga gct gtc atg ggg aac ttt ggt cag ggt     243
Gly Arg Gly Val Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly
          65             70             75

agt ttt gaa acc aca act gaa gca aca gac ctt gct att ggt ggt cgt     291
Ser Phe Glu Thr Thr Thr Glu Ala Thr Asp Leu Ala Ile Gly Gly Arg
          80             85             90

gga ttt ttc aaa gtt aaa cca caa gga tca gag act tca tat tat acc     339
Gly Phe Phe Lys Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr
          95             100             105

cgt gca ggt aat ttt cgt ttt aat aat gat gga tac tta gtt gat cct     387
Arg Ala Gly Asn Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro
          110             115             120

cat gga tat gct ctt cag ggt tgg aaa att gat aat act gaa ggg cca     435
His Gly Tyr Ala Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro
          125             130             135             140

caa cgt atc tca ggt ggt gtt aat cca ggt aca aat act tcg cag att     483

```

Gln Arg Ile Ser Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile	
145 150 155	
atg ggt aca ggt gaa cca aca gat atc cgt ctt gat act tgg aca gtt	531
Met Gly Thr Gly Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val	
160 165 170	
gca cct tta cag aca aca aat gta agt ttt aac gta aac ctt tct tct	579
Ala Pro Leu Gln Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser	
175 180 185	
gat aaa tct gga gat aaa tct caa aac gtt aat agt cca ttt acc tca	627
Asp Lys Ser Gly Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser	
190 195 200	
tta ttt aat ata tgg aat ggt aaa caa cca agt gaa cct aac aat cca	675
Leu Phe Asn Ile Trp Asn Gly Lys Gln Pro Ser Glu Pro Asn Asn Pro	
205 210 215 220	
cct atg cct gaa agt gca tat agt tat cag aca tct att aag gta tat	723
Pro Met Pro Glu Ser Ala Tyr Ser Tyr Gln Thr Ser Ile Lys Val Tyr	
225 230 235	
gat gaa gct ggt gga aca cat aca tta aca gtc tat ttt gac caa gtt	771
Asp Glu Ala Gly Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val	
240 245 250	
tct cct aaa gac tac aaa ggt ggt gga agt gga gaa agt gta tgg gaa	819
Ser Pro Lys Asp Tyr Lys Gly Gly Gly Ser Gly Glu Ser Val Trp Glu	
255 260 265	
tac gtt gtt act atg gat cct tct gaa gat aat cgc caa gtt tct gtt	867
Tyr Val Val Thr Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val	
270 275 280	
ggt ggt aac att gtg gac atc aaa gat act aaa gct gca gga atg tta	915
Gly Gly Asn Ile Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu	
285 290 295 300	
atg tca gga aca ttg agt ttt gat agc tca gga aaa ctt gca aac caa	963
Met Ser Gly Thr Leu Ser Phe Asp Ser Ser Gly Lys Leu Ala Asn Gln	
305 310 315	
agt gca tat tcg ctg aat ggt tca cgt aag cct gca gtt gat cct gca	1011
Ser Ala Tyr Ser Leu Asn Gly Ser Arg Lys Pro Ala Val Asp Pro Ala	
320 325 330	
acc gga gct ctt att aat ggt aat ggt ttt act att gat aga gat gga	1059
Thr Gly Ala Leu Ile Asn Gly Asn Gly Phe Thr Ile Asp Arg Asp Gly	
335 340 345	
aat gca att cct att ctt aat ata gat aat cca gct gaa aac ttc tat	1107
Asn Ala Ile Pro Ile Leu Asn Ile Asp Asn Pro Ala Glu Asn Phe Tyr	
350 355 360	
cca gca gaa gtt tct aat aat gga ttt cct atg att gta gct aat ttt	1155
Pro Ala Glu Val Ser Asn Asn Gly Phe Pro Met Ile Val Ala Asn Phe	
365 370 375 380	
act ggt gtc cca ggt aaa aat aca gct gga tct gtt ggt gat gct acc	1203
Thr Gly Val Pro Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr	
385 390 395	
acc ttt ttt aca gaa att gac ttt ggt tta aaa gct act gat ctt gat	1251
Thr Phe Phe Thr Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp	

400	405	410	
aat aca tgg aag aat gca aat gaa cct ctt tct tct tta agc tat aaa Asn Thr Trp Lys Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys 415 420 425			1299
aaa aca cat aat cct atg gat gtc gca ggt ggt tgg aca gtt ggt ggg Lys Thr His Asn Pro Met Asp Val Ala Gly Gly Trp Thr Val Gly Gly 430 435 440			1347
tat aaa act cca gct cca tca gta act gaa ctt ggt atg gct cag ata Tyr Lys Thr Pro Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile 445 450 455 460			1395
ttg gaa aat cct gct ggg gta atg cca caa tat tat ttt ggt aac cct Leu Glu Asn Pro Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro 465 470 475			1443
aac tat gat aac aca gtt cca cag agt cca cca tat gta tat aaa aat Asn Tyr Asp Asn Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn 480 485 490			1491
gaa gct tct tat cag gct gca tat aag act gca tta act gcc gca ggt Glu Ala Ser Tyr Gln Ala Ala Tyr Lys Thr Ala Leu Thr Ala Ala Gly 495 500 505			1539
ggg acc gca gct gac att aaa aag gaa cat tgg cct cat aat gct gca Gly Thr Ala Ala Asp Ile Lys Lys Glu His Trp Pro His Asn Ala Ala 510 515 520			1587
tca ggt ata tta gaa gct aat gat cca cca aat gtt aaa gac tta gct Ser Gly Ile Leu Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala 525 530 535 540			1635
aat atg aat gga aca cca aac cgc tta tca aat gcg ttt act aac tat Asn Met Asn Gly Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr 545 550 555			1683
gca ggt ggt agc tct aca aaa tct gca agt caa aat ggt tat ggt ttt Ala Gly Gly Ser Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe 560 565 570			1731
ggg gat tta atg aac tat agt gta aat gct gag gga gtg tta ttt gga Gly Asp Leu Met Asn Tyr Ser Val Asn Ala Glu Gly Val Leu Phe Gly 575 580 585			1779
gta tat tca aat gga gta caa ctt cca tta tat caa gta gct ctt tat Val Tyr Ser Asn Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr 590 595 600			1827
gat ttt aac tct aaa cag ggg tta cgt cgt gaa ggt ggt aac tta ttt Asp Phe Asn Ser Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe 605 610 615 620			1875
agt caa aca aga gaa tca ggg gac cca tct tca ggt gct gca aac act Ser Gln Thr Arg Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr 625 630 635			1923
tct ggg ttt ggt tca att aac gct aat act tta gaa gga tca aac gta Ser Gly Phe Gly Ser Ile Asn Ala Asn Thr Leu Glu Gly Ser Asn Val 640 645 650			1971
gat ata tct aca gag ttt gtc tca atg att gca aca caa cgt gga ttc Asp Ile Ser Thr Glu Phe Val Ser Met Ile Ala Thr Gln Arg Gly Phe 655 660 665			2019

cag tca aat agt aaa att gta act act att gac caa atg tta gag aca 2067
 Gln Ser Asn Ser Lys Ile Val Thr Thr Ile Asp Gln Met Leu Glu Thr
 670 675 680

gtt gta aat atg aag cgt tag 2088
 Val Val Asn Met Lys Arg
 685 690

<210> 2
 <211> 690
 <212> PRT
 <213> Lawsonia intracellularis

<400> 2

Met Ser Leu Thr Ala Gly Met Trp Thr Gly Val Ser Gly Leu Leu Ser
 1 5 10 15

His Gly Glu Lys Met Asn Val Ile Gly Asn Asn Ile Ala Asn Val Asn
 20 25 30

Thr Val Gly Phe Lys Gly Gln Arg Met Asp Phe Ala Asp Phe Ile Tyr
 35 40 45

Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile Gly Arg Gly Val
 50 55 60

Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly Ser Phe Glu Thr
 65 70 75 80

Thr Thr Glu Ala Thr Asp Leu Ala Ile Gly Gly Arg Gly Phe Phe Lys
 85 90 95

Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr Arg Ala Gly Asn
 100 105 110

Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro His Gly Tyr Ala
 115 120 125

Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro Gln Arg Ile Ser
 130 135 140

Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile Met Gly Thr Gly
 145 150 155 160

Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val Ala Pro Leu Gln
 165 170 175

Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser Asp Lys Ser Gly
 180 185 190

Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser Leu Phe Asn Ile
 195 200 205

Trp Asn Gly Lys Gln Pro Ser Glu Pro Asn Asn Pro Pro Met Pro Glu
 210 215 220

Ser Ala Tyr Ser Tyr Gln Thr Ser Ile Lys Val Tyr Asp Glu Ala Gly
 225 230 235 240

Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val Ser Pro Lys Asp
 245 250 255

Tyr Lys Gly Gly Gly Ser Gly Glu Ser Val Trp Glu Tyr Val Val Thr
 260 265 270

Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val Gly Gly Asn Ile
 275 280 285

Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu Met Ser Gly Thr
 290 295 300

Leu Ser Phe Asp Ser Ser Gly Lys Leu Ala Asn Gln Ser Ala Tyr Ser
 305 310 315 320

Leu Asn Gly Ser Arg Lys Pro Ala Val Asp Pro Ala Thr Gly Ala Leu
 325 330 335

Ile Asn Gly Asn Gly Phe Thr Ile Asp Arg Asp Gly Asn Ala Ile Pro
 340 345 350

Ile Leu Asn Ile Asp Asn Pro Ala Glu Asn Phe Tyr Pro Ala Glu Val
 355 360 365

Ser Asn Asn Gly Phe Pro Met Ile Val Ala Asn Phe Thr Gly Val Pro
 370 375 380

Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr Thr Phe Phe Thr
 385 390 395 400

Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp Asn Thr Trp Lys
 405 410 415

Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys Lys Thr His Asn
 420 425 430

Pro Met Asp Val Ala Gly Gly Trp Thr Val Gly Gly Tyr Lys Thr Pro
 435 440 445

Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile Leu Glu Asn Pro

450 455 460
 Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro Asn Tyr Asp Asn
 465 470 475 480
 Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn Glu Ala Ser Tyr
 485 490 495
 Gln Ala Ala Tyr Lys Thr Ala Leu Thr Ala Ala Gly Gly Thr Ala Ala
 500 505 510
 Asp Ile Lys Lys Glu His Trp Pro His Asn Ala Ala Ser Gly Ile Leu
 515 520 525
 Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala Asn Met Asn Gly
 530 535 540
 Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr Ala Gly Gly Ser
 545 550 555 560
 Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe Gly Asp Leu Met
 565 570 575
 Asn Tyr Ser Val Asn Ala Glu Gly Val Leu Phe Gly Val Tyr Ser Asn
 580 585 590
 Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr Asp Phe Asn Ser
 595 600 605
 Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe Ser Gln Thr Arg
 610 615 620
 Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr Ser Gly Phe Gly
 625 630 635 640
 Ser Ile Asn Ala Asn Thr Leu Glu Gly Ser Asn Val Asp Ile Ser Thr
 645 650 655
 Glu Phe Val Ser Met Ile Ala Thr Gln Arg Gly Phe Gln Ser Asn Ser
 660 665 670
 Lys Ile Val Thr Thr Ile Asp Gln Met Leu Glu Thr Val Val Asn Met
 675 680 685
 Lys Arg
 690
 <210> 3
 <211> 751

<212> DNA

<213> *Lawsonia intracellularis*

<220>

<221> CDS

<222> (32)..(715)

<400> 3

```

aagagttacc ctacggttag gagctaacaa c atg ttt cgt atg att gtt ttt      52
                               Met Phe Arg Met Ile Val Phe
                               1           5

ttt act gta ggt atc att atg ctt att ctt gct tgc tta gct gca ctt      100
Phe Thr Val Gly Ile Ile Met Leu Ile Leu Ala Cys Leu Ala Ala Leu
      10           15           20

gag ttc ata caa gat ttt ccc aat agc tat caa gaa gat gga caa atg      148
Glu Phe Ile Gln Asp Phe Pro Asn Ser Tyr Gln Glu Asp Gly Gln Met
      25           30           35

gtt aca gga att att tca aaa ata ata ggc tct aac tgt gat aat tct      196
Val Thr Gly Ile Ile Ser Lys Ile Ile Gly Ser Asn Cys Asp Asn Ser
      40           45           50           55

tca aca tct gat ata aat aat aag aaa tcc ata gat aga gat aaa gat      244
Ser Thr Ser Asp Ile Asn Asn Lys Lys Ser Ile Asp Arg Asp Lys Asp
      60           65           70

aca tta ctc tca agt agt aat aga aat aca ata caa gcc ggt act cca      292
Thr Leu Leu Ser Ser Ser Asn Arg Asn Thr Ile Gln Ala Gly Thr Pro
      75           80           85

cat caa gaa aat aac ata aaa gaa gat ctt caa ctg act aac aaa aat      340
His Gln Glu Asn Asn Ile Lys Glu Asp Leu Gln Leu Thr Asn Lys Asn
      90           95           100

gaa caa aca act cca gaa gaa gaa gaa gaa agt aaa ttt att tgg tta      388
Glu Gln Thr Thr Pro Glu Glu Glu Glu Glu Ser Lys Phe Ile Trp Leu
      105           110           115

aca gaa gct cca tca gag ctt aaa aaa gga gaa aaa gct ata aca caa      436
Thr Glu Ala Pro Ser Glu Leu Lys Lys Gly Glu Lys Ala Ile Thr Gln
      120           125           130           135

aca aga ttg tct att ggt aag gat ata tct ttt aga att act gct gat      484
Thr Arg Leu Ser Ile Gly Lys Asp Ile Ser Phe Arg Ile Thr Ala Asp
      140           145           150

gat gcc atc aaa gct caa tca atg atg tta aaa aat cca gat agg ttt      532
Asp Ala Ile Lys Ala Gln Ser Met Met Leu Lys Asn Pro Asp Arg Phe
      155           160           165

gtt tta gat ctt caa gga aag tgg ggt att tcc ctt cca cct att cca      580
Val Leu Asp Leu Gln Gly Lys Trp Gly Ile Ser Leu Pro Pro Ile Pro
      170           175           180

cct aca aat cct tgg tta aaa aaa ata cgc tta ggt act aat aat gga      628
Pro Thr Asn Pro Trp Leu Lys Lys Ile Arg Leu Gly Thr Asn Asn Gly
      185           190           195

aat aca cga ctt gtc ttt gat ctt caa aaa aaa cca tct aaa act gaa      676
Asn Thr Arg Leu Val Phe Asp Leu Gln Lys Lys Pro Ser Lys Thr Glu
      200           205           210           215

```

att aaa caa tta gat aca aat aaa att gaa atc caa att cattaaattg 725
 Ile Lys Gln Leu Asp Thr Asn Lys Ile Glu Ile Gln Ile
 220 225

catattagac aataagttat aataaaa 751

<210> 4
 <211> 228
 <212> PRT
 <213> Lawsonia intracellularis

<400> 4

Met Phe Arg Met Ile Val Phe Phe Thr Val Gly Ile Ile Met Leu Ile
 1 5 10 15

Leu Ala Cys Leu Ala Ala Leu Glu Phe Ile Gln Asp Phe Pro Asn Ser
 20 25 30

Tyr Gln Glu Asp Gly Gln Met Val Thr Gly Ile Ile Ser Lys Ile Ile
 35 40 45

Gly Ser Asn Cys Asp Asn Ser Ser Thr Ser Asp Ile Asn Asn Lys Lys
 50 55 60

Ser Ile Asp Arg Asp Lys Asp Thr Leu Leu Ser Ser Ser Asn Arg Asn
 65 70 75 80

Thr Ile Gln Ala Gly Thr Pro His Gln Glu Asn Asn Ile Lys Glu Asp
 85 90 95

Leu Gln Leu Thr Asn Lys Asn Glu Gln Thr Thr Pro Glu Glu Glu Glu
 100 105 110

Glu Ser Lys Phe Ile Trp Leu Thr Glu Ala Pro Ser Glu Leu Lys Lys
 115 120 125

Gly Glu Lys Ala Ile Thr Gln Thr Arg Leu Ser Ile Gly Lys Asp Ile
 130 135 140

Ser Phe Arg Ile Thr Ala Asp Asp Ala Ile Lys Ala Gln Ser Met Met
 145 150 155 160

Leu Lys Asn Pro Asp Arg Phe Val Leu Asp Leu Gln Gly Lys Trp Gly
 165 170 175

Ile Ser Leu Pro Pro Ile Pro Pro Thr Asn Pro Trp Leu Lys Lys Ile
 180 185 190

Arg Leu Gly Thr Asn Asn Gly Asn Thr Arg Leu Val Phe Asp Leu Gln
 195 200 205

Lys Lys Pro Ser Lys Thr Glu Ile Lys Gln Leu Asp Thr Asn Lys Ile
 210 215 220

Glu Ile Gln Ile
 225

<210> 5
 <211> 1715
 <212> DNA
 <213> Lawsonia intracellularis

<220>
 <221> CDS
 <222> (34)..(1677)

<400> 5
 aagcttttggg aatagtttct aaggagttat tta atg cat caa aaa agt tgt tta 54
 Met His Gln Lys Ser Cys Leu
 1 5

gtt gct tta tgt att atg ttt att att atg gtg caa gtt ctt cag gca 102
 Val Ala Leu Cys Ile Met Phe Ile Ile Met Val Gln Val Leu Gln Ala
 10 15 20

aat gca gct agc tat gtg gtt ttg cca ttt aaa gta aat gct cct cca 150
 Asn Ala Ala Ser Tyr Val Val Leu Pro Phe Lys Val Asn Ala Pro Pro
 25 30 35

agc tat act tat ttg gaa aaa gct atc cca tct atg tta act tct aga 198
 Ser Tyr Thr Tyr Leu Glu Lys Ala Ile Pro Ser Met Leu Thr Ser Arg
 40 45 50 55

ctt tat tgg gaa gaa cgt ttt caa cct atc ccg gat gct aat gct att 246
 Leu Tyr Trp Glu Glu Arg Phe Gln Pro Ile Pro Asp Ala Asn Ala Ile
 60 65 70

aaa gca gga aag gta gaa gat ata aag gaa atg gat aag gca agg ata 294
 Lys Ala Gly Lys Val Glu Asp Ile Lys Glu Met Asp Lys Ala Arg Ile
 75 80 85

gct aca ggt gca gac tat ctt ata tgg gga cag gta aat att gta ggt 342
 Ala Thr Gly Ala Asp Tyr Leu Ile Trp Gly Gln Val Asn Ile Val Gly
 90 95 100

gat gaa gct acg ctt gat gta caa gtt tgt gat ata gaa gga tca att 390
 Asp Glu Ala Thr Leu Asp Val Gln Val Cys Asp Ile Glu Gly Ser Ile
 105 110 115

tgg agg aaa agt aaa aat aca aaa gtt gat aat tta att act gcc ctt 438
 Trp Arg Lys Ser Lys Asn Thr Lys Val Asp Asn Leu Ile Thr Ala Leu
 120 125 130 135

caa gat aca gca gat gca att aat agt gag ttg ttt ggg cgt gca act 486
 Gln Asp Thr Ala Asp Ala Ile Asn Ser Glu Leu Phe Gly Arg Ala Thr
 140 145 150

aca aaa cca tca tca aaa gct act att gta gct caa atg aac tct gga 534
 Thr Lys Pro Ser Ser Lys Ala Thr Ile Val Ala Gln Met Asn Ser Gly
 155 160 165

ttg att aag gga aaa gga aat gaa aat cag tca tat ctt aat cca gaa 582

Leu Ile Lys Gly Lys Gly Asn Glu Asn Gln Ser Tyr Leu Asn Pro Glu	
170 175 180	
ttt cgt tat caa gga agc aat ctt tcc cgt ggc cga agt caa gct ctt	630
Pro Arg Tyr Gln Gly Ser Asn Leu Ser Arg Gly Arg Ser Gln Ala Leu	
185 190 195	
ccc ttt gct tca gtt ggt ata gtt gtt ggt gac ttt ata gga gat aat	678
Pro Phe Ala Ser Val Gly Ile Val Val Gly Asp Phe Ile Gly Asp Asn	
200 205 210 215	
aaa aat gaa gtt gcc ata tta agt gag tat aaa gtc cat att tat cga	726
Lys Asn Glu Val Ala Ile Leu Ser Glu Tyr Lys Val His Ile Tyr Arg	
220 225 230	
tgg gaa gaa gaa agg tta gct ctt ctt gga gaa tat aaa ttc cct cgc	774
Trp Glu Glu Glu Arg Leu Ala Leu Leu Gly Glu Tyr Lys Phe Pro Arg	
235 240 245	
tca cta cag tct tta cat att cgt gct ttt gat gtg gat cat gat ggt	822
Ser Leu Gln Ser Leu His Ile Arg Ala Phe Asp Val Asp His Asp Gly	
250 255 260	
gta cag gaa atc att gtt tct tgc ttt gat cct tca tat gca aag cca	870
Val Gln Glu Ile Ile Val Ser Cys Phe Asp Pro Ser Tyr Ala Lys Pro	
265 270 275	
tat tgc ttt att ctt agt ttt aaa aat aga gtg ttt aaa gag tta gcc	918
Tyr Ser Phe Ile Leu Ser Phe Lys Asn Arg Val Phe Lys Glu Leu Ala	
280 285 290 295	
aca aac tta cca ttt tat tta aat gtg gtt aaa ctt cca cca gat ttt	966
Thr Asn Leu Pro Phe Tyr Leu Asn Val Val Lys Leu Pro Pro Asp Phe	
300 305 310	
tct cct atg tta att ggt caa aag agt gac aat tca agg att ttt tct	1014
Ser Pro Met Leu Ile Gly Gln Lys Ser Asp Asn Ser Arg Ile Phe Ser	
315 320 325	
ccc tct ggg gtt tat gaa ata gaa aaa cat gga cgt aac tat ata atg	1062
Pro Ser Gly Val Tyr Glu Ile Glu Lys His Gly Arg Asn Tyr Ile Met	
330 335 340	
gga aat cgt ctt agt ctt cca aag gaa gct aat att ttt aat ttt tct	1110
Gly Asn Arg Leu Ser Leu Pro Lys Glu Ala Asn Ile Phe Asn Phe Ser	
345 350 355	
tgg tta cca tca gat tca tta aaa gat gaa gaa gct aag tta gta ctt	1158
Trp Leu Pro Ser Asp Ser Leu Lys Asp Glu Glu Ala Lys Leu Val Leu	
360 365 370 375	
gta acc aat aat gaa aga tta gtt gta tat aat aca aaa ggt aca aga	1206
Val Thr Asn Asn Glu Arg Leu Val Val Tyr Asn Thr Lys Gly Thr Arg	
380 385 390	
ctt ttt atg act gaa gaa gtg tat tat ggt tct tct gtt ggt ata gac	1254
Leu Phe Met Thr Glu Glu Val Tyr Tyr Gly Ser Ser Val Gly Ile Asp	
395 400 405	
gag ccc agt aat atg cct ggt ctt gga aag tca aaa gag ctt atc cct	1302
Glu Pro Ser Asn Met Pro Gly Leu Gly Lys Ser Lys Glu Leu Ile Pro	
410 415 420	
tct aaa tat ttt atc cca gga cgg atg att cct att aat ctt gat tca	1350
Ser Lys Tyr Phe Ile Pro Gly Arg Met Ile Pro Ile Asn Leu Asp Ser	

425 430 435
 atg ggg aaa tgg gag ttg ctt gta agc aag cca att tct gtt gca gca 1398
 Met Gly Lys Trp Glu Leu Leu Val Ser Lys Pro Ile Ser Val Ala Ala
 440 445 450 455
 aaa ttt ttt gaa aat tat aga tct ttt gct gaa ggc gaa att cag gct 1446
 Lys Phe Phe Glu Asn Tyr Arg Ser Phe Ala Glu Gly Glu Ile Gln Ala
 460 465 470
 tta aca tgg gac ggc tta gga tta ggt ctt gta tgg aat aca cgt cgt 1494
 Leu Thr Trp Asp Gly Leu Gly Leu Gly Leu Val Trp Asn Thr Arg Arg
 475 480 485
 att aag gga act att aca gat ttt gcc tta gct gat atg aat aat gat 1542
 Ile Lys Gly Thr Ile Thr Asp Phe Ala Leu Ala Asp Met Asn Asn Asp
 490 495 500
 ggg aag tta gac tta gtt gtt tcc gtt aat agc cat aca ggg att ctt 1590
 Gly Lys Leu Asp Leu Val Val Ser Val Asn Ser His Thr Gly Ile Leu
 505 510 515
 gga cta gaa aaa cga aag aca att ata gta ttt tat cct tta gag gta 1638
 Gly Leu Glu Lys Arg Lys Thr Ile Ile Val Phe Tyr Pro Leu Glu Val
 520 525 530 535
 gat aaa caa ggt atc cct aag gct gtt gaa gat aac taa ttttttccta 1687
 Asp Lys Gln Gly Ile Pro Lys Ala Val Glu Asp Asn
 540 545
 ttaattattt ttttattctg atagttaa 1715

 <210> 6
 <211> 547
 <212> PRT
 <213> *Lawsonia intracellularis*

 <400> 6
 Met His Gln Lys Ser Cys Leu Val Ala Leu Cys Ile Met Phe Ile Ile
 1 5 10 15
 Met Val Gln Val Leu Gln Ala Asn Ala Ala Ser Tyr Val Val Leu Pro
 20 25 30
 Phe Lys Val Asn Ala Pro Pro Ser Tyr Thr Tyr Leu Glu Lys Ala Ile
 35 40 45
 Pro Ser Met Leu Thr Ser Arg Leu Tyr Trp Glu Glu Arg Phe Gln Pro
 50 55 60
 Ile Pro Asp Ala Asn Ala Ile Lys Ala Gly Lys Val Glu Asp Ile Lys
 65 70 75 80
 Glu Met Asp Lys Ala Arg Ile Ala Thr Gly Ala Asp Tyr Leu Ile Trp
 85 90 95
 Gly Gln Val Asn Ile Val Gly Asp Glu Ala Thr Leu Asp Val Gln Val

100	105	110
Cys Asp Ile Glu Gly Ser Ile Trp Arg Lys Ser Lys Asn Thr Lys Val 115 120 125		
Asp Asn Leu Ile Thr Ala Leu Gln Asp Thr Ala Asp Ala Ile Asn Ser 130 135 140		
Glu Leu Phe Gly Arg Ala Thr Thr Lys Pro Ser Ser Lys Ala Thr Ile 145 150 155 160		
Val Ala Gln Met Asn Ser Gly Leu Ile Lys Gly Lys Gly Asn Glu Asn 165 170 175		
Gln Ser Tyr Leu Asn Pro Glu Phe Arg Tyr Gln Gly Ser Asn Leu Ser 180 185 190		
Arg Gly Arg Ser Gln Ala Leu Pro Phe Ala Ser Val Gly Ile Val Val 195 200 205		
Gly Asp Phe Ile Gly Asp Asn Lys Asn Glu Val Ala Ile Leu Ser Glu 210 215 220		
Tyr Lys Val His Ile Tyr Arg Trp Glu Glu Glu Arg Leu Ala Leu Leu 225 230 235 240		
Gly Glu Tyr Lys Phe Pro Arg Ser Leu Gln Ser Leu His Ile Arg Ala 245 250 255		
Phe Asp Val Asp His Asp Gly Val Gln Glu Ile Ile Val Ser Cys Phe 260 265 270		
Asp Pro Ser Tyr Ala Lys Pro Tyr Ser Phe Ile Leu Ser Phe Lys Asn 275 280 285		
Arg Val Phe Lys Glu Leu Ala Thr Asn Leu Pro Phe Tyr Leu Asn Val 290 295 300		
Val Lys Leu Pro Pro Asp Phe Ser Pro Met Leu Ile Gly Gln Lys Ser 305 310 315 320		
Asp Asn Ser Arg Ile Phe Ser Pro Ser Gly Val Tyr Glu Ile Glu Lys 325 330 335		
His Gly Arg Asn Tyr Ile Met Gly Asn Arg Leu Ser Leu Pro Lys Glu 340 345 350		
Ala Asn Ile Phe Asn Phe Ser Trp Leu Pro Ser Asp Ser Leu Lys Asp 355 360 365		

Glu Glu Ala Lys Leu Val Leu Val Thr Asn Asn Glu Arg Leu Val Val
370 375 380

Tyr Asn Thr Lys Gly Thr Arg Leu Phe Met Thr Glu Glu Val Tyr Tyr
385 390 395 400

Gly Ser Ser Val Gly Ile Asp Glu Pro Ser Asn Met Pro Gly Leu Gly
405 410 415

Lys Ser Lys Glu Leu Ile Pro Ser Lys Tyr Phe Ile Pro Gly Arg Met
420 425 430

Ile Pro Ile Asn Leu Asp Ser Met Gly Lys Trp Glu Leu Leu Val Ser
435 440 445

Lys Pro Ile Ser Val Ala Ala Lys Phe Phe Glu Asn Tyr Arg Ser Phe
450 455 460

Ala Glu Gly Glu Ile Gln Ala Leu Thr Trp Asp Gly Leu Gly Leu Gly
465 470 475 480

Leu Val Trp Asn Thr Arg Arg Ile Lys Gly Thr Ile Thr Asp Phe Ala
485 490 495

Leu Ala Asp Met Asn Asn Asp Gly Lys Leu Asp Leu Val Val Ser Val
500 505 510

Asn Ser His Thr Gly Ile Leu Gly Leu Glu Lys Arg Lys Thr Ile Ile
515 520 525

Val Phe Tyr Pro Leu Glu Val Asp Lys Gln Gly Ile Pro Lys Ala Val
530 535 540

Glu Asp Asn
545

<210> 7
<211> 1564
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (41)..(1522)

<400> 7
agaagtatgt tctataagta gagtaaggaa tataaaaaaat atg gtt agt tat att
Met Val Ser Tyr Ile
1 5

cgt tta tta gga agt ata ttt tta gta tta gca att ttt ggt tgt ggc Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala Ile Phe Gly Cys Gly 10 15 20	103
gct cag ttt aat aaa ccc tct tta ctt gat gaa acc cct ata gat tac Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu Thr Pro Ile Asp Tyr 25 30 35	151
agt tct gta ctt tct gat tac ata gta gaa tta gaa aaa gaa cca ctt Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu Glu Lys Glu Pro Leu 40 45 50	199
cag tat ata tta cta aaa aaa gaa aaa ttt tct caa atg gag ata tat Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser Gln Met Glu Ile Tyr 55 60 65	247
aat tat caa ttc aca tca caa cat tgg tct cca gat aat ttt gta tca Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro Asp Asn Phe Val Ser 70 75 80 85	295
cct gct ata tgg gaa cat cag gta gat ata tat atc cct cac cat cca Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr Ile Pro His His Pro 90 95 100	343
gtt tca gaa cgt gca ctt ctt atc atc aat aat ggt att aat aat ggt Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn Gly Ile Asn Asn Gly 105 110 115	391
aca ttt ttt act tct cct aaa gct cca act gat ttt act cca gaa gta Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp Phe Thr Pro Glu Val 120 125 130	439
tta gaa gaa atc gct cgt tca aca aaa act gta gtc att gct cta agt Leu Glu Glu Ile Ala Arg Ser Thr Lys Thr Val Val Ile Ala Leu Ser 135 140 145	487
gat atc cca aat cag tat ctt act tat aga ggt gac tgg aga ttt ctt Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly Asp Trp Arg Phe Leu 150 155 160 165	535
aag gaa gat gaa agt att gct atg agt tgg tct agt ttt tta caa gat Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser Ser Phe Leu Gln Asp 170 175 180	583
cca gaa agt cgg tac aca aga cct ctc tat gtc cct atg gtt gca gca Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val Pro Met Val Ala Ala 185 190 195	631
gtt tct cag gca atg act ctt gca gaa aag gag tta caa gca tta aaa Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu Leu Gln Ala Leu Lys 200 205 210	679
att aag cat ttt att gta tct ggt gtg tca aag cgt gga tgg aca aca Ile Lys His Phe Ile Val Ser Gly Val Ser Lys Arg Gly Trp Thr Thr 215 220 225	727
tgg ctt tca gct att gct gac tca cga gta gat gct att acc ccg ttt Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp Ala Ile Thr Pro Phe 230 235 240 245	775
gtt att gat gca ttg aat act cgg aaa gtc ctt gga cat atg tat aaa Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu Gly His Met Tyr Lys 250 255 260	823
aca tat gga aat aat tgg cct ata gca ttt tat cca tat tat aga ttt	871

Thr Tyr Gly Asn Asn Trp Pro Ile Ala Phe Tyr Pro Tyr Tyr Arg Phe
 265 270 275
 gat tta gat aaa caa cta gat aca gtt cct ttt ttc aat ctt atg aat 919
 Asp Leu Asp Lys Gln Leu Asp Thr Val Pro Phe Phe Asn Leu Met Asn
 280 285 290
 att gtt gat cca tat aga tat tta gga aca cca tat aag tct cga ctt 967
 Ile Val Asp Pro Tyr Arg Tyr Leu Gly Thr Pro Tyr Lys Ser Arg Leu
 295 300 305
 gct atc cct aaa tat att gta aat gca agt gga gat gat ttt tat gtc 1015
 Ala Ile Pro Lys Tyr Ile Val Asn Ala Ser Gly Asp Asp Phe Tyr Val
 310 315 320 325
 cct gat aat tca agt ttt tac tat gat gat ctc cct gga gag aaa gca 1063
 Pro Asp Asn Ser Ser Phe Tyr Tyr Asp Asp Leu Pro Gly Glu Lys Ala
 330 335 340
 tta cgt ttt gca cca aac tca aat cat cat ggg ata tta aat ttc aca 1111
 Leu Arg Phe Ala Pro Asn Ser Asn His His Gly Ile Leu Asn Phe Thr
 345 350 355
 aaa caa tgc ctt att cct ttt gtg aat aga gta caa aaa ggt att tca 1159
 Lys Gln Ser Leu Ile Pro Phe Val Asn Arg Val Gln Lys Gly Ile Ser
 360 365 370
 acg cca gtt tta gat att tcc aca gag atg acg gaa cga gtt caa tat 1207
 Thr Pro Val Leu Asp Ile Ser Thr Glu Met Thr Glu Arg Val Gln Tyr
 375 380 385
 gtg act gtt cgt ttt tct gaa gtt cca gag aag ata gta ctt tgg aaa 1255
 Val Thr Val Arg Phe Ser Glu Val Pro Glu Lys Ile Val Leu Trp Lys
 390 395 400 405
 gca gca aat cca gag tca cga gat ttt cgt tat gcc tgt cgt gtt agg 1303
 Ala Ala Asn Pro Glu Ser Arg Asp Phe Arg Tyr Ala Cys Arg Val Arg
 410 415 420
 tac atg gaa aca cca tta cac ctt tct gca aca ggg gaa gtt agc gtt 1351
 Tyr Met Glu Thr Pro Leu His Leu Ser Ala Thr Gly Glu Val Ser Val
 425 430 435
 tca tta gag atc cct tct gta gga tgg caa gct gct ttt att gaa gct 1399
 Ser Leu Glu Ile Pro Ser Val Gly Trp Gln Ala Ala Phe Ile Glu Ala
 440 445 450
 aca ttt aaa gat ggt ttt gtt gca aca aca cca gtg tat att tta cca 1447
 Thr Phe Lys Asp Gly Phe Val Ala Thr Thr Pro Val Tyr Ile Leu Pro
 455 460 465
 aaa gat ata tat cca cct ata aaa ata cca cct gta cat gga tta tta 1495
 Lys Asp Ile Tyr Pro Pro Ile Lys Ile Pro Pro Val His Gly Leu Leu
 470 475 480 485
 tgt aag ttt gta cat ggt cga acc tag taactagtag ttgttgtact 1542
 Cys Lys Phe Val His Gly Arg Thr
 490
 gataatctaa aaggatatag at 1564

<210> 8
 <211> 493
 <212> PRT

<213> Lawsonia intracellularis

<400> 8

Met Val Ser Tyr Ile Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala
1 5 10 15

Ile Phe Gly Cys Gly Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu
20 25 30

Thr Pro Ile Asp Tyr Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu
35 40 45

Glu Lys Glu Pro Leu Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser
50 55 60

Gln Met Glu Ile Tyr Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro
65 70 75 80

Asp Asn Phe Val Ser Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr
85 90 95

Ile Pro His His Pro Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn
100 105 110

Gly Ile Asn Asn Gly Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp
115 120 125

Phe Thr Pro Glu Val Leu Glu Glu Ile Ala Arg Ser Thr Lys Thr Val
130 135 140

Val Ile Ala Leu Ser Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly
145 150 155 160

Asp Trp Arg Phe Leu Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser
165 170 175

Ser Phe Leu Gln Asp Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val
180 185 190

Pro Met Val Ala Ala Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu
195 200 205

Leu Gln Ala Leu Lys Ile Lys His Phe Ile Val Ser Gly Val Ser Lys
210 215 220

Arg Gly Trp Thr Thr Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp
225 230 235 240

Ala Ile Thr Pro Phe Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu

<210>	9
<211>	2096

<212> DNA
 <213> *Lawsonia intracellularis*

<220>
 <221> CDS
 <222> (12)..(2096)

<400> 9
 aggacaaaac t atg gcg gat tat ctt tca gga gga att tct ttt gga gga 50
 Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly
 1 5 10

att ggt agt gga acc gat ttc caa gct atg att gat caa ctt aag aaa 98
 Ile Gly Ser Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys
 15 20 25

att gag ctt att cct aaa aat aga ctt gta gtt tcc cat gaa caa tgg 146
 Ile Glu Leu Ile Pro Lys Asn Arg Leu Val Ser His Glu Gln Trp
 30 35 40 45

aca aaa aaa tat aaa gca ttt gaa gag ctt ata aaa aca gtt aaa gat 194
 Thr Lys Lys Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp
 50 55 60

act gaa gcg tct tta agt aag cta agt tct gtt ggt gct att tta aaa 242
 Thr Glu Ala Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys
 65 70 75

aaa gaa ggt tct gtt tca aat act tct gtt gca agc gtt aag gca agt 290
 Lys Glu Gly Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser
 80 85 90

tct gat gca tct gat gga aca cat aca att gat gtg aaa cag ctt gca 338
 Ser Asp Ala Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala
 95 100 105

aca aac acg att ctt tct aat aat cat att ttt gat tct aaa act gaa 386
 Thr Asn Thr Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu
 110 115 120 125

agt att aat aat aca ggt tca cct ggt atc ttt gct tat gag tat aaa 434
 Ser Ile Asn Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys
 130 135 140

ggg gaa cta cat gaa gtt gaa gtt cct cca ggt agt gat ctt gaa tat 482
 Gly Glu Leu His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr
 145 150 155

ctt gca aca tta ata aac aaa gat tct aat aat cct ggt gtt aaa gca 530
 Leu Ala Thr Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala
 160 165 170

aac ctt atc aag act ggc gat ggc tat atg ttt agt ctt gaa gga act 578
 Asn Leu Ile Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr
 175 180 185

gaa act ggt gca aat gcg act tta tct att tca aat aag aca acg ctt 626
 Glu Thr Gly Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu
 190 195 200 205

cca gac ttt aaa gca tct gtt gct acc agc agt gca tta gct aat ggt 674
 Pro Asp Phe Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly
 210 215 220

gaa gat aca att att aat act tca gga aca act caa caa ttt tct ttt Glu Asp Thr Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe 225 230 235	722
gaa tac aat gga aga aca ttt act ttc gat att cct tca gga aca aca Glu Tyr Asn Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr 240 245 250	770
gca aaa gaa ctc caa aca gct ata aat gaa aat aca aaa aat aca gga Ala Lys Glu Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly 255 260 265	818
gta cgt gca act ttt gaa aaa cat ggc tca gat ata gta ttg caa tta Val Arg Ala Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu 270 275 280 285	866
gaa gga aca gtt cct aat caa caa gtt aaa gta acc gct agc cct act Glu Gly Thr Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr 290 295 300	914
gat ctt gga agt ttc aca tct tcg ggt caa gca ggc tgg aat aaa cgt Asp Leu Gly Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg 305 310 315	962
gat tct caa gat gct att ttt aat att aat ggt tgg gac caa gaa ctt Asp Ser Gln Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu 320 325 330	1010
aca tct tct aca aat gaa ctt aca gaa gtt atc cca gga ctt caa att Thr Ser Ser Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile 335 340 345	1058
aca cta ctt tcc gaa ggg aaa aca caa att aca att cag act tct act Thr Leu Leu Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr 350 355 360 365	1106
gac gaa gta aaa aaa caa gtt gag aaa gca gta gag tct ata aat aat Asp Glu Val Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn 370 375 380	1154
gtt ctt tcc aaa att caa gag tta act aaa gca aca gct gaa gac aaa Val Leu Ser Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys 385 390 395	1202
gat gat agt aaa gac act tct agt tct tca agt aaa att cca tca tat Asp Asp Ser Lys Asp Thr Ser Ser Ser Ser Ser Lys Ile Pro Ser Tyr 400 405 410	1250
tta caa agt cct aca aaa gtg aag gct gga cta ttt aca ggt gat act Leu Gln Ser Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr 415 420 425	1298
ggc ata caa atg ctt agt act aga ctt aag tct atc ttt tct tct aat Gly Ile Gln Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn 430 435 440 445	1346
ggt cta ggt ttt tct cct aaa caa aca caa gat ggt cca ggg gat cta Gly Leu Gly Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu 450 455 460	1394
ttt tca tca ctt gct tca att ggt att gtc gta gat gct gat gag ggt Phe Ser Ser Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly 465 470 475	1442
agt gaa act ttt gga caa ctt aaa att tta gat aga gaa aca att ggt	1490

Ser Glu Thr Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly
 480 485 490
 cct gat gca cct tat aca act ctt gat gag gca tta aaa aaa gat cca 1538
 Pro Asp Ala Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro
 495 500 505
 caa gca gta gca gat ata tta gct ggt agt tct gga ata tct gat tca 1586
 Gln Ala Val Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser
 510 515 520 525
 aca gat ttt tct tat caa gat cat att gtt gga aaa aca caa gct ggt 1634
 Thr Asp Phe Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly
 530 535 540
 aca tat gat gta aag tat tct gta gat gca agt ggt act ata gga gac 1682
 Thr Tyr Asp Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp
 545 550 555
 gtt tac att gga ggt gta aaa gct tct cta tct gat cct gca aaa aat 1730
 Val Tyr Ile Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn
 560 565 570
 ata tat acg gtc aca tct ggt cct gct aca ggt ctt agt ata gca gtt 1778
 Ile Tyr Thr Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val
 575 580 585
 aat aat cgt act cca ggt atc aat gta gaa agt act gta aga gtc aaa 1826
 Asn Asn Arg Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys
 590 595 600 605
 caa ggt aaa ctt agc caa ata caa gaa gca ctt aaa gct gaa gta cag 1874
 Gln Gly Lys Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln
 610 615 620
 caa gat cct tta aaa gaa aac aca ggt cct tta att atc atg caa gat 1922
 Gln Asp Pro Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp
 625 630 635
 aac tat aag gat gtt atg aaa aat ctt gag aca aga ata gaa aaa gaa 1970
 Asn Tyr Lys Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu
 640 645 650
 aca caa aga gtt act agt tgg gaa cgt atg atg cgt tta aaa ttt tct 2018
 Thr Gln Arg Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser
 655 660 665
 aga ctt gat gct gta tta gca aaa tat aat cag atg atg tca gca aat 2066
 Arg Leu Asp Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn
 670 675 680 685
 gct tct agt tta ggg caa ctt ggt gca taa 2096
 Ala Ser Ser Leu Gly Gln Leu Gly Ala
 690

<210> 10
 <211> 694
 <212> PRT
 <213> Lawsonia intracellularis

<400> 10

Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly Ile Gly Ser
 1 5 10 15

Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys Ile Glu Leu
 20 25 30
 Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp Thr Lys Lys
 35 40 45
 Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp Thr Glu Ala
 50 55 60
 Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys Lys Glu Gly
 65 70 75 80
 Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser Ser Asp Ala
 85 90 95
 Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala Thr Asn Thr
 100 105 110
 Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu Ser Ile Asn
 115 120 125
 Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys Gly Glu Leu
 130 135 140
 His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr Leu Ala Thr
 145 150 155 160
 Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala Asn Leu Ile
 165 170 175
 Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr Glu Thr Gly
 180 185 190
 Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu Pro Asp Phe
 195 200 205
 Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly Glu Asp Thr
 210 215 220
 Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe Glu Tyr Asn
 225 230 235 240
 Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr Ala Lys Glu
 245 250 255
 Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly Val Arg Ala
 260 265 270

Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu Glu Gly Thr
 275 280 285
 Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr Asp Leu Gly
 290 295 300
 Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg Asp Ser Gln
 305 310 315 320
 Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu Thr Ser Ser
 325 330 335
 Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile Thr Leu Leu
 340 345 350
 Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr Asp Glu Val
 355 360 365
 Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn Val Leu Ser
 370 375 380
 Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys Asp Asp Ser
 385 390 395 400
 Lys Asp Thr Ser Ser Ser Ser Ser Lys Ile Pro Ser Tyr Leu Gln Ser
 405 410 415
 Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr Gly Ile Gln
 420 425 430
 Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn Gly Leu Gly
 435 440 445
 Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu Phe Ser Ser
 450 455 460
 Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly Ser Glu Thr
 465 470 475 480
 Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly Pro Asp Ala
 485 490 495
 Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro Gln Ala Val
 500 505 510
 Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser Thr Asp Phe
 515 520 525

Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly Thr Tyr Asp
530 535 540

Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp Val Tyr Ile
545 550 555 560

Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn Ile Tyr Thr
565 570 575

Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val Asn Asn Arg
580 585 590

Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys Gln Gly Lys
595 600 605

Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln Gln Asp Pro
610 615 620

Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp Asn Tyr Lys
625 630 635 640

Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu Thr Gln Arg
645 650 655

Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser Arg Leu Asp
660 665 670

Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn Ala Ser Ser
675 680 685

Leu Gly Gln Leu Gly Ala
690

<210> 11
<211> 1200
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (13)..(1200)

<400> 11
taggagatag tt atg gct aat gtt agt gga atc cct gca cca cga tta ctt 51
Met Ala Asn Val Ser Gly Ile Pro Ala Pro Arg Leu Leu
1 5 10

tcc aca aca aat caa atg acc aat gca gct gct ggt aat act aat aga 99
Ser Thr Thr Asn Gln Met Thr Asn Ala Ala Gly Asn Thr Asn Arg
15 20 25

gct acc ggt agt atg aac ggt cgt aat ctc aca caa ata aaa aca cct 147
Ala Thr Gly Ser Met Asn Gly Arg Asn Leu Thr Gln Ile Lys Thr Pro

30	35	40	45	
cag tcc atg att gat aat gct tca gaa gaa tta aca act tct ctt gaa				195
Gln Ser Met Ile Asp Asn Ala Ser Glu Glu Leu Thr Thr Ser Leu Glu	50	55	60	
tct aaa agc agt gac gac ttt gca att aaa gat cgt aaa aga caa ggg				243
Ser Lys Ser Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln Gly	65	70	75	
aaa gga tct gat tct cta tta aaa atg gtt caa gaa tat aca gag ctg				291
Lys Gly Ser Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu Leu	80	85	90	
acg aat gat gat acc cgt aat gct aaa aga gct atg tta tcc cag gta				339
Thr Asn Asp Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln Val	95	100	105	
tta cgt gca agt caa agt tca caa gat gta ctc gaa aaa aca tta gaa				387
Leu Arg Ala Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu Glu	110	115	120	125
caa ttt tct aat aaa aca gat gct tgg gct tct ctt gca gaa att gca				435
Gln Phe Ser Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala	130	135	140	
caa gaa tat ggt gca gaa tct cca cag cca aca gga tta aaa tct gta				483
Gln Glu Tyr Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val	145	150	155	
tta gat gct atg gag aca tta gaa aat gag ttt ggt gat gaa att aaa				531
Leu Asp Ala Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys	160	165	170	
gca gga cta aaa gga gct cta aat tca aaa gaa ttt act gat ata ggc				579
Ala Gly Leu Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly	175	180	185	
agt gca gca cag tta aga gat ctt tat aca aca aca gta act ata aca				627
Ser Ala Ala Gln Leu Arg Asp Leu Tyr Thr Thr Thr Val Thr Ile Thr	190	195	200	205
gct gca cct gat gca gtg tta gca aga ctt ctt gaa gaa tat gag agt				675
Ala Ala Pro Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser	210	215	220	
gat gat gat ctg gat aga gcc att gat ttc ctt cta tct aca ctt ggt				723
Asp Asp Asp Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly	225	230	235	
gga gag ctt gaa tca gct gat cca agt atg gat aaa gta cat ctt Caa				771
Gly Glu Leu Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu Gln	240	245	250	
agt gta atg ggt gat att gaa aaa aca caa caa ctt cat agc tct Cat				819
Ser Val Met Gly Asp Ile Glu Lys Thr Gln Gln Leu His Ser Ser His	255	260	265	
aaa caa tgt act aca gcc ctt agc agg tgg aaa gag aaa cat aaa ggt				867
Lys Gln Cys Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys Gly	270	275	280	285
ggg ggg gaa aat agt aca cta act cct tta gaa atg atg cgt gaa cta				915
Gly Gly Glu Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg Glu Leu	290	295	300	

att gca cta aaa aat gaa aat ttt att tct cct tcc tct ata gat aaa 963
 Ile Ala Leu Lys Asn Glu Asn Phe Ile Ser Pro Ser Ser Ile Asp Lys
 305 310 315

att gtt gat caa gct gat ccc caa gat att gaa aaa gaa gtc ctt ttt 1011
 Ile Val Asp Gln Ala Asp Pro Gln Asp Ile Glu Lys Glu Val Leu Phe
 320 325 330

tta caa gag atg tta gct gct gta aga aaa ttt ccc att atg gta ttt 1059
 Leu Gln Glu Met Leu Ala Ala Val Arg Lys Phe Pro Ile Met Val Phe
 335 340 345

gat aat gtc gaa aat cgt gta aga gtt atg ggt gct gta caa gat gct 1107
 Asp Asn Val Glu Asn Arg Val Arg Val Met Gly Ala Val Gln Asp Ala
 350 355 360 365

gtt gac gat gct gta aga aga gaa gat gaa ttc ctc ttt caa aaa gaa 1155
 Val Asp Asp Ala Val Arg Arg Glu Asp Glu Phe Leu Phe Gln Lys Glu
 370 375 380

cat cct gat gta cca cta caa cca gat gaa aat aat ata caa taa 1200
 His Pro Asp Val Pro Leu Gln Pro Asp Glu Asn Asn Ile Gln
 385 390 395

<210> 12
 <211> 395
 <212> PRT
 <213> Lawsonia intracelluláris

<400> 12

Met Ala Asn Val Ser Gly Ile Pro Ala Pro Arg Leu Leu Ser Thr Thr
 1 5 10 15

Asn Gln Met Thr Asn Ala Ala Ala Gly Asn Thr Asn Arg Ala Thr Gly
 20 25 30

Ser Met Asn Gly Arg Asn Leu Thr Gln Ile Lys Thr Pro Gln Ser Met
 35 40 45

Ile Asp Asn Ala Ser Glu Glu Leu Thr Thr Ser Leu Glu Ser Lys Ser
 50 55 60

Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln Gly Lys Gly Ser
 65 70 75 80

Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu Leu Thr Asn Asp
 85 90 95

Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln Val Leu Arg Ala
 100 105 110

Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu Glu Gln Phe Ser
 115 120 125

Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala Gln Glu Tyr
 130 135 140

Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val Leu Asp Ala
 145 150 155 160

Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys Ala Gly Leu
 165 170 175

Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly Ser Ala Ala
 180 185 190

Gln Leu Arg Asp Leu Tyr Thr Thr Thr Val Thr Ile Thr Ala Ala Pro
 195 200 205

Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser Asp Asp Asp
 210 215 220

Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly Gly Glu Leu
 225 230 235 240

Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu Gln Ser Val Met
 245 250 255

Gly Asp Ile Glu Lys Thr Gln Gln Leu His Ser Ser His Lys Gln Cys
 260 265 270

Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys Gly Gly Gly Glu
 275 280 285

Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg Glu Leu Ile Ala Leu
 290 295 300

Lys Asn Glu Asn Phe Ile Ser Pro Ser Ser Ile Asp Lys Ile Val Asp
 305 310 315 320

Gln Ala Asp Pro Gln Asp Ile Glu Lys Glu Val Leu Phe Leu Gln Glu
 325 330 335

Met Leu Ala Ala Val Arg Lys Phe Pro Ile Met Val Phe Asp Asn Val
 340 345 350

Glu Asn Arg Val Arg Val Met Gly Ala Val Gln Asp Ala Val Asp Asp
 355 360 365

Ala Val Arg Arg Glu Asp Glu Phe Leu Phe Gln Lys Glu His Pro Asp
 370 375 380

Val Pro Leu Gln Pro Asp Glu Asn Asn Ile Gln

385

390

395

```
<210> 13
<211> 1269
<212> DNA
<213> Lawsonia intracellularis
```

```
<220>
<221> CDS
<222> (32) .. (1222)
```

```

<400> 13
tggttgaaat tctctctgga ggagtaaagc a atg aca aat ttt gga gat ata      52
          Met Thr Asn Phe Gly Asp Ile
                1             5

```

agc gga agc tcc gca aga atg agt agc ttg atg act ggt aca tcc ggt 100
 Ser Gly Ser Ser Ala Arg Met Ser Ser Leu Met Thr Gly Thr Ser Gly
 10 15 20

gaa gaa gga ctt gaa gaa ctt gaa ggt ggt gtt cct aaa gag caa ggt 148
Glu Glu Gly Leu Glu Glu Leu Glu Gly Gly Val Pro Lys Glu Gln Gly
25 30 35

ggt cca ggt aaa gga gat gct tca gag gct gct aaa ggt caa gca gca 196
Gly Pro Gly Lys Gly Asp Ala Ser Glu Ala Ala Lys Gly Gln Ala Ala
40 45 50 55

gca gat agt att aat tca gct ggt ggt act gaa aag cct gga gaa gtt 244
Ala Asp Ser Ile Asn Ser Ala Gly Gly Thr Glu Lys Pro Gly Glu Val
60 65 70

ggt gat aag gaa gat gta ggg gaa ggt ggc gaa ata cct gaa ggt ggt 292
Gly Asp Lys Glu Asp Val Gly Glu Gly Gly Glu Ile Pro Glu Gly Gly
75 80 85

gaa ata cct gag ggt ggt gaa gaa gtt cca gag gaa ccc cca tat gtc 340
Glu Ile Pro Glu Gly Gly Glu Glu Val Pro Glu Glu Pro Pro Tyr Val
90 95 100

cct cct cca ttg gtt gaa cca gct aaa atc agt aca gta aca gat ctc 388
Pro Pro Pro Leu Val Glu Pro Ala Lys Ile Ser Thr Val Thr Asp Leu
105 110 115

agt acg tta atg gga tca cta cag ctg aca gag caa aaa aag aat gct 436
Ser Thr Leu Met Gly Ser Leu Gln Leu Thr Glu Gln Lys Lys Asn Ala
120 125 130 135

gaa aaa aca gta aat gaa att aaa gca cag aat aaa gag caa caa gta 484
Glu Lys Thr Val Asn Glu Ile Lys Ala Gln Asn Lys Glu Gln Gln Val
140 145 150

aag ttc caa gag caa att aaa aag att gag gat aat att gct gaa tct 532
Lys Phe Gln Glu Gln Ile Lys Lys Ile Glu Asp Asn Ile Ala Glu Ser
155 160 165

aag aaa agt ggt ata ctt aag ttt ttc caa aag ttg ttt gca gtt att 580
Lys Lys Ser Gly Ile Leu Lys Phe Phe Gln Lys Leu Phe Ala Val Ile
170 175 180

ggt gct gta cta gga gct att gga ggt gcg cta gct att gct gca ggt 628
Gly Ala Val Leu Gly Ala Ile Gly Gly Ala Leu Ala Ile Ala Ala Gly
185 190 195

gct gct tca ggt aac cca tta ttg gtt gct gca ggt att atg gct att 676
 Ala Ala Ser Gly Asn Pro Leu Leu Val Ala Ala Gly Ile Met Ala Ile
 200 205 210 215

gta gct tca att gat gca gca atg tcg tct cta tcg gat ggt aaa gtg 724
 Val Ala Ser Ile Asp Ala Ala Met Ser Ser Leu Ser Asp Gly Lys Val
 220 225 230

tcc atc tca gca ggg att agt aag gct ctt gag gct atg gga gta cca 772
 Ser Ile Ser Ala Gly Ile Ser Lys Ala Leu Glu Ala Met Gly Val Pro
 235 240 245

gca gaa aca gca caa tgg att gca ttt ggt ata cag tta gca atg att 820
 Ala Glu Thr Ala Gln Trp Ile Ala Phe Gly Ile Gln Leu Ala Met Ile
 250 255 260

gca gtg act ata gct att ggt ttt gcc tct ggt ggt ggt gga gca atg 868
 Ala Val Thr Ile Ala Ile Gly Phe Ala Ser Gly Gly Gly Gly Ala Met
 265 270 275

gct gga gtg tca aaa ata gca gat atg ttt tca aag tct caa gat gta 916
 Ala Gly Val Ser Lys Ile Ala Asp Met Phe Ser Lys Ser Gln Asp Val
 280 285 290 295

gct aag ttg gca cag atg att gaa aaa gct tct aaa ata gta caa atc 964
 Ala Lys Leu Ala Gln Met Ile Glu Lys Ala Ser Lys Ile Val Gln Ile
 300 305 310

gct ggt tca gtt aat cag tct gct ata ggc ggt aca ggt att ggt aca 1012
 Ala Gly Ser Val Asn Gln Ser Ala Ile Gly Gly Thr Gly Ile Gly Thr
 315 320 325

gct gta gtg caa agc aat ata aaa gct aat gaa tct gaa caa aaa gaa 1060
 Ala Val Val Gln Ser Asn Ile Lys Ala Asn Glu Ser Glu Gln Lys Glu
 330 335 340

att gaa gct gct att gca aaa gtt aaa gct aag ata gag acg tta caa 1108
 Ile Glu Ala Ala Ile Ala Lys Val Lys Ala Lys Ile Glu Thr Leu Gln
 345 350 355

gac ttc ttt aaa aac caa atg gaa caa ttc aat gct ata atg aaa ata 1156
 Asp Phe Phe Lys Asn Gln Met Glu Gln Phe Asn Ala Ile Met Lys Ile
 360 365 370 375

ata aca gat att att caa gat agc gtc aat aca aaa ata gct gtt caa 1204
 Ile Thr Asp Ile Ile Gln Asp Ser Val Asn Thr Lys Ile Ala Val Gln
 380 385 390

cgt ggt gca cgt gag taa taacttagt aaat acagtg actatactat 1252
 Arg Gly Ala Arg Glu
 395

aatatataaa ttaataa 1269

<210> 14
 <211> 396
 <212> PRT
 <213> Lawsonia intracellularis

<400> 14

Met Thr Asn Phe Gly Asp Ile Ser Gly Ser Ser Ala Arg Met Ser Ser
 1 5 10 15

Leu Met Thr Gly Thr Ser Gly Glu Glu Gly Leu Glu Glu Leu Glu Gly
 20 25 30

Gly Val Pro Lys Glu Gln Gly Gly Pro Gly Lys Gly Asp Ala Ser Glu
 35 40 45

Ala Ala Lys Gly Gln Ala Ala Ala Asp Ser Ile Asn Ser Ala Gly Gly
 50 55 60

Thr Glu Lys Pro Gly Glu Val Gly Asp Lys Glu Asp Val Gly Glu Gly
 65 70 75 80

Gly Glu Ile Pro Glu Gly Gly Glu Ile Pro Glu Gly Gly Glu Glu Val
 85 90 95

Pro Glu Glu Pro Pro Tyr Val Pro Pro Pro Leu Val Glu Pro Ala Lys
 100 105 110

Ile Ser Thr Val Thr Asp Leu Ser Thr Leu Met Gly Ser Leu Gln Leu
 115 120 125

Thr Glu Gln Lys Lys Asn Ala Glu Lys Thr Val Asn Glu Ile Lys Ala
 130 135 140

Gln Asn Lys Glu Gln Gln Val Lys Phe Glu Glu Gln Ile Lys Lys Ile
 145 150 155 160

Glu Asp Asn Ile Ala Glu Ser Lys Lys Ser Gly Ile Leu Lys Phe Phe
 165 170 175

Gln Lys Leu Phe Ala Val Ile Gly Ala Val Leu Gly Ala Ile Gly Gly
 180 185 190

Ala Leu Ala Ile Ala Ala Gly Ala Ala Ser Gly Asn Pro Leu Leu Val
 195 200 205

Ala Ala Gly Ile Met Ala Ile Val Ala Ser Ile Asp Ala Ala Met Ser
 210 215 220

Ser Leu Ser Asp Gly Lys Val Ser Ile Ser Ala Gly Ile Ser Lys Ala
 225 230 235 240

Leu Glu Ala Met Gly Val Pro Ala Glu Thr Ala Gln Trp Ile Ala Phe
 245 250 255

Gly Ile Gln Leu Ala Met Ile Ala Val Thr Ile Ala Ile Gly Phe Ala
 260 265 270

Ser Gly Gly Gly Gly Ala Met Ala Gly Val Ser Lys Ile Ala Asp Met
275 280 285

Phe Ser Lys Ser Gln Asp Val Ala Lys Leu Ala Gln Met Ile Glu Lys
290 295 300

Ala Ser Lys Ile Val Gln Ile Ala Gly Ser Val Asn Gln Ser Ala Ile
305 310 315 320

Gly Gly Thr Gly Ile Gly Thr Ala Val Val Gln Ser Asn Ile Lys Ala
325 330 335

Asn Glu Ser Glu Gln Lys Glu Ile Glu Ala Ala Ile Ala Lys Val Lys
340 345 350

Ala Lys Ile Glu Thr Leu Gln Asp Phe Phe Lys Asn Gln Met Glu Gln
355 360 365

Phe Asn Ala Ile Met Lys Ile Ile Thr Asp Ile Ile Gln Asp Ser Val
370 375 380

Asn Thr Lys Ile Ala Val Gln Arg Gly Ala Arg Glu
385 390 395

<210> 15
<211> 894
<212> DNA
<213> *Lawsonia intracellularis*

<220>
<221> CDS
<222> (13)..(894)

<400> 15
aggaggaatt at atg tct ctt gtc att aat aac aac ctg atg gcc gtc aat 51
Met Ser Leu Val Ile Asn Asn Asn Leu Met Ala Val Asn
1 5 10
gct caa cgt aac tta agc aag tct tat gga gaa ctg agt tct tct gtt 99
Ala Gln Arg Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val
15 20 25
cga aaa ctt tct tca ggt ctt cgt gta gga act gct gct gat gac tca 147
Arg Lys Leu Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser
30 35 40 45
gca ggg tta gcc att cga gaa ctc atg aga tct gac att gca aca aca 195
Ala Gly Leu Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr
50 55 60
caa caa gga ata cga aat gcg aat gat gct att tct atg att caa act 243
Gln Gln Gly Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr
65 70 75
gcg gat ggt gca ctt gga gtc atc gat gaa aag ctc att cga atg aaa 291

Ala Asp Gly Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys
80 85 90
gaa ctt gct gaa caa gct gct aca ggt aca tat aac tcc act cag cgt 339
Glu Leu Ala Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg
95 100 105
atg att att gac tct gaa tat caa gct atg gcc tca gaa att act cgt 387
Met Ile Ile Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg
110 115 120 125
att gct aat gcg aca gaa ttt aat ggt ata aaa ctt ctt gat ggt tca 435
Ile Ala Asn Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser
130 135 140
tta tca ggt aat cat gat ggg aaa aaa ata aat tca act ggt gca gta 483
Leu Ser Gly Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val
145 150 155
cgt atc cac ttt ggg aca tct aac agc tct gct gaa gat tac tat gat 531
Arg Ile His Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp
160 165 170
att aaa att ggt ggc tct aca gct tct gca tta gga ctt ggt aat aca 579
Ile Lys Ile Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr
175 180 185
gta aaa ggt gcg ggt gct aca gtc tct act caa gct gca gca caa aat 627
Val Lys Gly Ala Gly Ala Thr Val Ser Thr Gln Ala Ala Ala Gln Asn
190 195 200 205
gcc tta aaa gct ata gat aat gcc att gtt tca aaa gat aaa att cga 675
Ala Leu Lys Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg
210 215 220
gca cac ctt ggt gga tta caa aat aga ctt gaa gct aca gtt gat aat 723
Ala His Leu Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn
225 230 235
tta agt ata caa aat gaa aac tta caa gct gct gaa tct cgt ata tct 771
Leu Ser Ile Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser
240 245 250
gat ata gat gta agc caa gaa atg aca caa ttt gta cgt aac caa ata 819
Asp Ile Asp Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile
255 260 265
ctt aca caa aca ggt gtt gct atg ctt tca caa gct aat tct cta cca 867
Leu Thr Gln Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro
270 275 280 285
cgt atg gct cag caa ctt att ggc taa 894
Arg Met Ala Gln Gln Leu Ile Gly
290

<210> 16
<211> 293
<212> PRT
<213> Lawsonia intracellularis

<400> 16

Met Ser Leu Val Ile Asn Asn Asn Leu Met Ala Val Asn Ala Gln Arg
1 5 10 15

Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val Arg Lys Leu
 20 25 30

Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser Ala Gly Leu
 35 40 45

Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr Gln Gln Gly
 50 55 60

Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr Ala Asp Gly
 65 70 75 80

Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys Glu Leu Ala
 85 90 95

Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg Met Ile Ile
 100 105 110

Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg Ile Ala Asn
 115 120 125

Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser Leu Ser Gly
 130 135 140

Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val Arg Ile His
 145 150 155 160

Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp Ile Lys Ile
 165 170 175

Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr Val Lys Gly
 180 185 190

Ala Gly Ala Thr Val Ser Thr Gln Ala Ala Ala Gln Asn Ala Leu Lys
 195 200 205

Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg Ala His Leu
 210 215 220

Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn Leu Ser Ile
 225 230 235 240

Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser Asp Ile Asp
 245 250 255

Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile Leu Thr Gln
 260 265 270

Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro Arg Met Ala
 275 280 285

Gln Gln Leu Ile Gly
 290

<210> 17
 <211> 2848
 <212> DNA
 <213> Lawsonia intracellularis

<220>
 <221> CDS
 <222> (29) .. (2848)

<400> 17
 accttaacta aaaaataaaa agaataatt atg tat aat ata att aat aag cat 52
 Met Tyr Asn Ile Ile Asn Lys His
 1 5

caa atc ata aaa att tta tta ttt tcc tta tgt gtt ttc ttt ttt aca 100
 Gln Ile Ile Lys Ile Leu Leu Phe Ser Leu Cys Val Phe Phe Phe Thr
 10 15 20

ctt aca gaa aaa caa aaa att tat gct gca gac gtc ttt ttt gag ggc 148
 Leu Thr Glu Lys Gln Lys Ile Tyr Ala Ala Asp Val Phe Phe Glu Gly
 25 30 35 40

aga acc gaa acc tta atc aat gta aac aaa cca ttt gat tct ttt ttt 196
 Arg Thr Glu Thr Leu Ile Asn Val Asn Lys Pro Phe Asp Ser Phe Phe
 45 50 55

gga ggt tct gac tct aca ata gga acc ctt gaa aca gga cct act aat 244
 Gly Gly Ser Asp Ser Thr Ile Gly Thr Leu Glu Thr Gly Pro Thr Asn
 60 65 70

ctt acc ttc aca aca gta gga gcc ttc cgc aat tct gtt ttc aga att 292
 Leu Thr Phe Thr Thr Val Gly Ala Phe Arg Asn Ser Val Phe Arg Ile
 75 80 85

att ggt ggt ggt agg tct agt ttt aac aac cca aat aca gtt aaa ggc 340
 Ile Gly Gly Gly Arg Ser Ser Phe Asn Asn Pro Asn Thr Val Lys Gly
 90 95 100

aat gtt act cta act gtt tat aat act gat gta gaa aga ata att ggt 388
 Asn Val Thr Leu Thr Val Tyr Asn Thr Asp Val Glu Arg Ile Ile Gly
 105 110 115 120

gca ggt atc agc aat aga gga ctt gta acc gtt act ggc tca gta aat 436
 Ala Gly Ile Ser Asn Arg Gly Leu Val Thr Val Thr Gly Ser Val Asn
 125 130 135

atg aag cta gaa aat gtt tct gtt act aga gga att tat ggt ggt gtc 484
 Met Lys Leu Glu Asn Val Ser Val Thr Arg Gly Ile Tyr Gly Gly Val
 140 145 150

tat act caa aat gga cat gta cta ggc tct atc aac atg cat ttg aaa 532
 Tyr Thr Gln Asn Gly His Val Leu Gly Ser Ile Asn Met His Leu Lys
 155 160 165

aac gtc caa act cca cta tta ata ggt tct gga gta agc aat gga cct 580

Asn Val Gln Thr Pro Leu Leu Ile Gly Ser Gly Val Ser Asn Gly Pro	
170 175 180	
aat cgt att act gta aat gga gac ata aac att gat gtt gaa gac tct	628
Asn Arg Ile Thr Val Asn Gly Asp Ile Asn Ile Asp Val Glu Asp Ser	
185 190 195 200	
agg att caa tat gta aac att aca gga gaa gta gat gca ggg ata aaa	676
Arg Ile Gln Tyr Val Asn Ile Thr Gly Glu Val Asp Ala Gly Ile Lys	
205 210 215	
gga aat gct act cta act gta aaa aaa tct act gtt gag ctt ata aac	724
Gly Asn Ala Thr Leu Thr Val Lys Lys Ser Thr Val Glu Leu Ile Asn	
220 225 230	
tct ggt aga ggt aat atc tta ggt aat ctc aaa ata tct ata gca gat	772
Ser Gly Arg Gly Asn Ile Leu Gly Asn Leu Lys Ile Ser Ile Ala Asp	
235 240 245	
tca aat ata agg ggg tta tca cca gta gac ttt ggt tct tca gta tat	820
Ser Asn Ile Arg Gly Leu Ser Pro Val Asp Phe Gly Ser Ser Val Tyr	
250 255 260	
ggg gac aca tct ata aat gta att aat tct cag att aat gat att act	868
Gly Asp Thr Ser Ile Asn Val Ile Asn Ser Gln Ile Asn Asp Ile Thr	
265 270 275 280	
ctt ata cca agg gct ggt gga atg ctt gta ggt cct gtt acc cta gat	916
Leu Ile Pro Arg Ala Gly Gly Met Leu Val Gly Pro Val Thr Leu Asp	
285 290 295	
atc aca agc agt act ata caa aat ata caa tgt ggg cct gtc agt caa	964
Ile Thr Ser Ser Thr Ile Gln Asn Ile Gln Cys Gly Pro Val Ser Gln	
300 305 310	
aat aat caa ctt aac aca cta aat gta act gtt aat act agt aac att	1012
Asn Asn Gln Leu Asn Thr Leu Asn Val Thr Val Asn Thr Ser Asn Ile	
315 320 325	
act aac tta aac ctt ggt agt gtc gaa ggt cat aca ata tca act aca	1060
Thr Asn Leu Asn Leu Gly Ser Val Glu Gly His Thr Ile Ser Thr Thr	
330 335 340	
gca act gtt act gat agt aat att act aac ctt aat gtc gga acc ttc	1108
Ala Thr Val Thr Asp Ser Asn Ile Thr Asn Leu Asn Val Gly Thr Phe	
345 350 355 360	
aat gga ctt gga gta act gag aat gcc tct gta atc att aat agt ggc	1156
Asn Gly Leu Gly Val Thr Glu Asn Ala Ser Val Ile Ile Asn Ser Gly	
365 370 375	
aat att act aac ctt aat gtc gga act aat gta ata gct gca gcc aca	1204
Asn Ile Thr Asn Leu Asn Val Gly Thr Asn Val Ile Ala Ala Thr	
380 385 390	
act att aat tcc tct gcg acc ata cac gac gga ctt att gca aac ctt	1252
Thr Ile Asn Ser Ser Ala Thr Ile His Asp Gly Leu Ile Ala Asn Leu	
395 400 405	
acc tta ggc tca caa ggt aat ggt cgt act atg ata gct aca gca aat	1300
Thr Leu Gly Ser Gln Gly Asn Gly Arg Thr Met Ile Ala Thr Ala Asn	
410 415 420	
gtt aat ggt gga act att gga tta tta act atg ggt tca gaa aac ttc	1348
Val Asn Gly Gly Thr Ile Gly Leu Leu Thr Met Gly Ser Glu Asn Phe	

425	430	435	440	
ata cca ggc aca aga cca att act gaa tta gca ata cta aac atg tct				1396
Ile Pro Gly Thr Arg Pro Ile Thr Glu Leu Ala Ile Leu Asn Met Ser	445	450	455	
ggg gga tta att gaa aga att atc gta ggt aat gcc aac tct tca acc				1444
Gly Gly Leu Ile Glu Arg Ile Ile Val Gly Asn Ala Asn Ser Ser Thr	460	465	470	
ata aac ttt act cct ggg aag aga tca att gta aaa aca ata aat ggt				1492
Ile Asn Phe Thr Pro Gly Lys Arg Ser Ile Val Lys Thr Ile Asn Gly	475	480	485	
cca gaa ctt cca tat tta gtt aac ata caa aaa ggt gct atg aca caa				1540
Pro Glu Leu Pro Tyr Leu Val Asn Ile Gln Lys Gly Ala Met Thr Gln	490	495	500	
tgg ggc act aaa aat atg ccc ttt tta ttg gat aca aga aat tta atc				1588
Trp Gly Thr Lys Asn Met Pro Phe Leu Leu Asp Thr Arg Asn Leu Ile	505	510	515	520
ttg tcc gga act ctg att acc tca aat att caa cta gct gat tta tct				1636
Leu Ser Gly Thr Leu Ile Thr Ser Asn Ile Gln Leu Ala Asp Leu Ser	525	530	535	
ata acc aat cta ttt gtt gct aat ggc ggt aca cta gta cct aga aaa				1684
Ile Thr Asn Leu Phe Val Ala Asn Gly Gly Thr Leu Val Pro Arg Lys	540	545	550	
tta ata cct ggg aac caa cct gtt ata cag ttt ctt gga ggt cct caa				1732
Leu Ile Pro Gly Asn Gln Pro Val Ile Gln Phe Leu Gly Gly Pro Gln	555	560	565	
tca ctc tta gtt atc cat caa cca tta aaa gta aat tta agc tta tca				1780
Ser Leu Leu Val Ile His Gln Pro Leu Lys Val Asn Leu Ser Leu Ser	570	575	580	
cca aaa ctt att gga agt agc atg gtg cca ctt gct ttt gtc tct caa				1828
Pro Lys Leu Ile Gly Ser Ser Met Val Pro Leu Ala Phe Val Ser Gln	585	590	595	600
tct ttt tca tca cca gat ctt ttt gtt aaa caa act aga agt ggt ctc				1876
Ser Phe Ser Ser Pro Asp Leu Phe Val Lys Gln Thr Arg Ser Gly Leu	605	610	615	
att tgg agt gat ctt gag ttt gat cca aca aca tct att tgg tat gtt				1924
Ile Trp Ser Asp Leu Glu Phe Asp Pro Thr Thr Ser Ile Trp Tyr Val	620	625	630	
aat aat atc caa gca tct caa gat ttt tac tct ttc tct att gct cgt				1972
Asn Asn Ile Gln Ala Ser Gln Asp Phe Tyr Ser Phe Ser Ile Ala Arg	635	640	645	
gag act act aac tgg cta aga caa caa cat ata tgg act cta caa aac				2020
Glu Thr Thr Asn Trp Leu Arg Gln Gln His Ile Trp Thr Leu Gln Asn	650	655	660	
cgt tca agt aaa ctt tta gac aac gaa cat tat gga cta tgg ata aat				2068
Arg Ser Ser Lys Leu Leu Asp Asn Glu His Tyr Gly Leu Trp Ile Asn	665	670	675	680
gtt caa ggt gga cat gaa agt ctt gat act tct att ggt agc aaa gca				2116
Val Gln Gly Gly His Glu Ser Leu Asp Thr Ser Ile Gly Ser Lys Ala	685	690	695	

aaa atg cca tgg ata atg gca aca gca gga tat gac tat ctt caa caa Lys Met Pro Trp Ile Met Ala Thr Ala Gly Tyr Asp Tyr Leu Gln Gln 700 705 710	2164
cta cca agg tta gat atg aaa gcc ctt tat ggt ctt gct ttt ggt gct Leu Pro Arg Leu Asp Met Lys Ala Leu Tyr Gly Leu Ala Phe Gly Ala 715 720 725	2212
tct aaa ggt aaa agt aaa tgg tct agc gtc aac tct aca aaa aat gat Ser Lys Gly Lys Ser Lys Trp Ser Ser Val Asn Ser Thr Lys Asn Asp 730 735 740	2260
gct gag cta ggt atg gtt agt ggt tat gta ggt ctt atc cat aac aaa Ala Glu Leu Gly Met Val Ser Gly Tyr Val Gly Leu Ile His Asn Lys 745 750 755 760	2308
act ggg ctc tat agt aca ttg acc tta caa ctt gcg tct agt aaa tta Thr Gly Leu Tyr Ser Thr Leu Thr Leu Gln Leu Ala Ser Ser Lys Leu 765 770 775	2356
cat act aat tct aca ggg ttc tat aga aat ttt aaa tgg aca gaa aca His Thr Asn Ser Thr Gly Phe Tyr Arg Asn Phe Lys Trp Thr Glu Thr 780 785 790	2404
act cca aca gaa gca ctt gaa ctt gga tgg aaa tac act ttc aac aac Thr Pro Thr Glu Ala Leu Glu Leu Gly Trp Lys Tyr Thr Phe Asn Asn 795 800 805	2452
ggg att aaa atg aat cct cgt gga caa ctt att ttt gaa caa aca tct Gly Ile Lys Met Asn Pro Arg Gly Gln Leu Ile Phe Glu Gln Thr Ser 810 815 820	2500
aaa cac cat ttt gat tta gga att caa aat gat aag gct ata tta gat Lys His His Phe Asp Leu Gly Ile Gln Asn Asp Lys Ala Ile Leu Asp 825 830 835 840	2548
aaa agc cag tta ata aca agt tct ctt ggt att acc gtt gaa tat aag Lys Ser Gln Leu Ile Thr Ser Ser Leu Gly Ile Thr Val Glu Tyr Lys 845 850 855	2596
cta cca gtt acc aca cct att aat ctt tat gct ggt att gaa agg ata Leu Pro Val Thr Thr Pro Ile Asn Leu Tyr Ala Gly Ile Glu Arg Ile 860 865 870	2644
aaa ggt cag tct gga aac ttt gca att agt tcc cag agc ctt caa atg Lys Gly Gln Ser Gly Asn Phe Ala Ile Ser Ser Gln Ser Leu Gln Met 875 880 885	2692
aag ttc aag cat gac aat gat aca agt gta gtt aga gca aca ata ggt Lys Phe Lys His Asp Asn Asp Thr Ser Val Val Arg Ala Thr Ile Gly 890 895 900	2740
aca aat ata tta ttg gga gaa cat ttt aat att cac tgt gat ata ttt Thr Asn Ile Leu Leu Gly Glu His Phe Asn Ile His Cys Asp Ile Phe 905 910 915 920	2788
gga gat aaa gga aat gat aaa ggc att ggt ggg caa gca gga ttt aca Gly Asp Lys Gly Asn Asp Lys Gly Ile Gly Gly Gln Ala Gly Phe Thr 925 930 935	2836
tac aaa ttt taa Tyr Lys Phe	2848

<210> 18
 <211> 939
 <212> PRT
 <213> Lawsonia intracellularis

<400> 18

Met Tyr Asn Ile Ile Asn Lys His Gln Ile Ile Lys Ile Leu Leu Phe
 1 5 10 15

Ser Leu Cys Val Phe Phe Phe Thr Leu Thr Glu Lys Gln Lys Ile Tyr
 20 25 30

Ala Ala Asp Val Phe Phe Glu Gly Arg Thr Glu Thr Leu Ile Asn Val
 35 40 45

Asn Lys Pro Phe Asp Ser Phe Phe Gly Gly Ser Asp Ser Thr Ile Gly
 50 55 60

Thr Leu Glu Thr Gly Pro Thr Asn Leu Thr Phe Thr Thr Val Gly Ala
 65 70 75 80

Phe Arg Asn Ser Val Phe Arg Ile Ile Gly Gly Gly Arg Ser Ser Phe
 85 90 95

Asn Asn Pro Asn Thr Val Lys Gly Asn Val Thr Leu Thr Val Tyr Asn
 100 105 110

Thr Asp Val Glu Arg Ile Ile Gly Ala Gly Ile Ser Asn Arg Gly Leu
 115 120 125

Val Thr Val Thr Gly Ser Val Asn Met Lys Leu Glu Asn Val Ser Val
 130 135 140

Thr Arg Gly Ile Tyr Gly Gly Val Tyr Thr Gln Asn Gly His Val Leu
 145 150 155 160

Gly Ser Ile Asn Met His Leu Lys Asn Val Gln Thr Pro Leu Leu Ile
 165 170 175

Gly Ser Gly Val Ser Asn Gly Pro Asn Arg Ile Thr Val Asn Gly Asp
 180 185 190

Ile Asn Ile Asp Val Glu Asp Ser Arg Ile Gln Tyr Val Asn Ile Thr
 195 200 205

Gly Glu Val Asp Ala Gly Ile Lys Gly Asn Ala Thr Leu Thr Val Lys
 210 215 220

Lys Ser Thr Val Glu Leu Ile Asn Ser Gly Arg Gly Asn Ile Leu Gly

225	230	235	240
Asn Leu Lys Ile Ser Ile Ala Asp Ser Asn Ile Arg Gly Leu Ser Pro	245	250	255
Val Asp Phe Gly Ser Ser Val Tyr Gly Asp Thr Ser Ile Asn Val Ile	260	265	270
Asn Ser Gln Ile Asn Asp Ile Thr Leu Ile Pro Arg Ala Gly Gly Met	275	280	285
Leu Val Gly Pro Val Thr Leu Asp Ile Thr Ser Ser Thr Ile Gln Asn	290	295	300
Ile Gln Cys Gly Pro Val Ser Gln Asn Asn Gln Leu Asn Thr Leu Asn	305	310	315
Val Thr Val Asn Thr Ser Asn Ile Thr Asn Leu Asn Leu Gly Ser Val	325	330	335
Glu Gly His Thr Ile Ser Thr Thr Ala Thr Val Thr Asp Ser Asn Ile	340	345	350
Thr Asn Leu Asn Val Gly Thr Phe Asn Gly Leu Gly Val Thr Glu Asn	355	360	365
Ala Ser Val Ile Ile Asn Ser Gly Asn Ile Thr Asn Leu Asn Val Gly	370	375	380
Thr Asn Val Ile Ala Ala Ala Thr Thr Ile Asn Ser Ser Ala Thr Ile	385	390	395
His Asp Gly Leu Ile Ala Asn Leu Thr Leu Gly Ser Gln Gly Asn Gly	405	410	415
Arg Thr Met Ile Ala Thr Ala Asn Val Asn Gly Gly Thr Ile Gly Leu	420	425	430
Leu Thr Met Gly Ser Glu Asn Phe Ile Pro Gly Thr Arg Pro Ile Thr	435	440	445
Glu Leu Ala Ile Leu Asn Met Ser Gly Gly Leu Ile Glu Arg Ile Ile	450	455	460
Val Gly Asn Ala Asn Ser Ser Thr Ile Asn Phe Thr Pro Gly Lys Arg	465	470	475
Ser Ile Val Lys Thr Ile Asn Gly Pro Glu Leu Pro Tyr Leu Val Asn	485	490	495

Ile Gln Lys Gly Ala Met Thr Gln Trp Gly Thr Lys Asn Met Pro Phe
 500 505 510

Leu Leu Asp Thr Arg Asn Leu Ile Leu Ser Gly Thr Leu Ile Thr Ser
 515 520 525

Asn Ile Gln Leu Ala Asp Leu Ser Ile Thr Asn Leu Phe Val Ala Asn
 530 535 540

Gly Gly Thr Leu Val Pro Arg Lys Leu Ile Pro Gly Asn Gln Pro Val
 545 550 555 560

Ile Gln Phe Leu Gly Gly Pro Gln Ser Leu Leu Val Ile His Gln Pro
 565 570 575

Leu Lys Val Asn Leu Ser Leu Ser Pro Lys Leu Ile Gly Ser Ser Met
 580 585 590

Val Pro Leu Ala Phe Val Ser Gln Ser Phe Ser Ser Pro Asp Leu Phe
 595 600 605

Val Lys Gln Thr Arg Ser Gly Leu Ile Trp Ser Asp Leu Glu Phe Asp
 610 615 620

Pro Thr Thr Ser Ile Trp Tyr Val Asn Asn Ile Gln Ala Ser Gln Asp
 625 630 635 640

Phe Tyr Ser Phe Ser Ile Ala Arg Glu Thr Thr Asn Trp Leu Arg Gln
 645 650 655

Gln His Ile Trp Thr Leu Gln Asn Arg Ser Ser Lys Leu Leu Asp Asn
 660 665 670

Glu His Tyr Gly Leu Trp Ile Asn Val Gln Gly Gly His Glu Ser Leu
 675 680 685

Asp Thr Ser Ile Gly Ser Lys Ala Lys Met Pro Trp Ile Met Ala Thr
 690 695 700

Ala Gly Tyr Asp Tyr Leu Gln Gln Leu Pro Arg Leu Asp Met Lys Ala
 705 710 715 720

Leu Tyr Gly Leu Ala Phe Gly Ala Ser Lys Gly Lys Ser Lys Trp Ser
 725 730 735

Ser Val Asn Ser Thr Lys Asn Asp Ala Glu Leu Gly Met Val Ser Gly
 740 745 750

Tyr Val Gly Leu Ile His Asn Lys Thr Gly Leu Tyr Ser Thr Leu Thr
 755 760 765
 Leu Gln Leu Ala Ser Ser Lys Leu His Thr Asn Ser Thr Gly Phe Tyr
 770 775 780
 Arg Asn Phe Lys Trp Thr Glu Thr Thr Pro Thr Glu Ala Leu Glu Leu
 785 790 795 800
 Gly Trp Lys Tyr Thr Phe Asn Asn Gly Ile Lys Met Asn Pro Arg Gly
 805 810 815
 Gln Leu Ile Phe Glu Gln Thr Ser Lys His His Phe Asp Leu Gly Ile
 820 825 830
 Gln Asn Asp Lys Ala Ile Leu Asp Lys Ser Gln Leu Ile Thr Ser Ser
 835 840 845
 Leu Gly Ile Thr Val Glu Tyr Lys Leu Pro Val Thr Thr Pro Ile Asn
 850 855 860
 Leu Tyr Ala Gly Ile Glu Arg Ile Lys Gly Gln Ser Gly Asn Phe Ala
 865 870 875 880
 Ile Ser Ser Gln Ser Leu Gln Met Lys Phe Lys His Asp Asn Asp Thr
 885 890 895
 Ser Val Val Arg Ala Thr Ile Gly Thr Asn Ile Leu Leu Gly Glu His
 900 905 910
 Phe Asn Ile His Cys Asp Ile Phe Gly Asp Lys Gly Asn Asp Lys Gly
 915 920 925
 Ile Gly Gly Gln Ala Gly Phe Thr Tyr Lys Phe
 930 935